

IN THE CLAIMS:

1. (Currently amended) An isolated nucleic acid molecule encoding a polypeptide having diacylglycerol acyltransferase activity, wherein the isolated nucleic acid molecule comprises a sequence encoding ~~[[a]]~~ the polypeptide of SEQ ID NO: 2.

2. (Currently amended) An isolated nucleic acid molecule encoding a polypeptide having diacylglycerol acyltransferase activity, wherein the isolated nucleic acid molecule comprises a sequence according to SEQ ID NO: 1~~[[,]]~~ or SEQ ID NO: 3~~, or a fragment of SEQ ID NO: 1 or SEQ ID NO: 3 having 90% identity with SEQ ID NO: 1 or SEQ ID NO: 3, wherein the fragment encodes the polypeptide having the diacylglycerol acyltransferase activity.~~

3. (Currently amended) A vector for transformation of plant cells, wherein said vector comprises a nucleic acid sequence encoding a polypeptide having diacylglycerol acyltransferase activity, wherein ~~[[a]]~~ the sequence of the polypeptide comprises SEQ ID NO: 2.

4. (Currently amended) A vector for transformation of plant cells, wherein said vector comprises a nucleic acid sequence encoding a polypeptide having diacylglycerol acyltransferase activity, wherein the nucleic acid sequence comprises SEQ ID NO: 1~~[[,]]~~ or SEQ ID NO: 3~~, or a fragment of SEQ ID NO: 1 or SEQ ID NO: 3 having 90% identity with SEQ ID NO: 1 or SEQ ID NO: 3, wherein the fragment encodes the a polypeptide having the diacylglycerol acyltransferase activity.~~

5. (Withdrawn). A vector for transformation of plant cells, wherein said vector contains a nucleic acid sequence according to SEQ ID NO: 23, which is SEQ ID NO: 1 altered to contain an 81 bp insertion, such that the deduced amino acid sequence of the encoded protein contains the repeated sequence SHAGLFNLCVVVLIHAVNSRLIENLMK according to SEQ ID NO: 25, where the spacing and identity of the G at position 4, the N at position 7, the V at position 10, the V at position 11, the L at position 13, the I at position 14, the N at position 17, the R at position 19, the L at position 20, the E at position 23, the N at position 24, the L at position 25 and the K at position 27 are identical or are replaced by conserved substitutions.

6. (Previously presented) The vector according to claim 3, wherein said nucleic acid sequence is present in said vector in a sense orientation.

7. (Withdrawn). A vector according to claim 3, characterized in that said sequence is present in said vector in an anti-sense orientation.

8. (Previously presented) Plasmid pDGATcDNA having accession number ATCC PTA-989.

9. (Previously presented) Plasmid pDGATgene having accession number ATCC PTA-988.

10. (Currently amended) A plant having a genome, wherein the genome comprises an introduced nucleotide sequence encoding a polypeptide having diacylglycerol acyltransferase activity, wherein the sequence of the polypeptide comprises SEQ ID NO: 2.

11. (Currently amended) A plant seed having a genome, wherein said genome comprises an introduced nucleotide sequence encoding a polypeptide having diacylglycerol acyltransferase activity, wherein the sequence of the polypeptide comprises SEQ ID NO: 2.

12. (Currently amended) A genetically transformed plant, wherein ~~[[a]]~~ the genome of the plant has been transformed by the vector according to claim 3 or claim 4.

13. (Currently amended) A genetically transformed plant seed, wherein ~~[[a]]~~ the genome of the plant seed has been transformed by the vector according to claim 3 or claim 4.

14. (Currently amended) The plant seed of Claim 11, wherein the plant seed exhibits an altered seed oil content compared to an average of a statistically-significant number of seeds of plants of the same genotype grown in identical conditions, but without the introduced nucleotide sequence ~~grown in identical conditions~~.

15. (Currently amended) The plant seed of Claim 11, wherein the plant seed exhibits an altered diacylglycerol content in its seed oil compared to an average of a statistically-significant number of seeds of plants of the same genotype grown in identical conditions, but without the introduced nucleotide sequence ~~grown in identical conditions~~.

16. (Currently amended) The plant seed of Claim 11, wherein the plant seed exhibits a seed oil with an altered fatty acyl composition compared to an average of a statistically-significant number of seeds of a plant of the same genotype grown in identical conditions, but without the introduced nucleotide sequence ~~grown in identical conditions~~.

17. (Currently amended) The plant of Claim 10, wherein a plant seed of the plant exhibits an enhanced biomass compared to an average of a statistically-significant number of plants of the same genotype grown in identical conditions, but without the introduced nucleotide sequence ~~grown in identical conditions~~.

18. (Currently amended) The plant seed of Claim 11, wherein the plant seed exhibits an enhanced biomass compared to an average of a statistically-significant number of seeds of plants of the same genotype grown in identical conditions, but without the introduced nucleotide sequence ~~grown under identical conditions~~.

19. (Currently amended) A method of producing transgenic plants comprising:
introducing a nucleotide sequence into ~~[[a]]~~ the genome of a plant;
wherein said nucleotide sequence introduced into said genome encodes a polypeptide having diacylglycerol acyltransferase activity, wherein ~~[[a]]~~ the sequence of the polypeptide comprises SEQ ID NO: 2.

20. (Previously presented) The method according to claim 19, wherein said plant is a member of the Brassicaceae.

21. (Currently amended) The method according to claim 19, wherein said plant is selected from the group consisting of *Arabidopsis thaliana*, *Borago* spp., Canola, *Ricinus* spp., *Theobroma* spp., *Zea* spp., *Gossypium* spp, *Crambe* spp., *Cuphea* spp., *Linum* spp., *Lesquerella* spp., *Limnanthes* spp., Linola, *Tropaeolum* spp., *Oenothera* spp., *Olea* spp., *Elaeis* spp., *Arachis* spp., rapeseed, *Carthamus* spp., *Glycine* spp., Soja spp., *Helianthus* spp., *Nicotiana* spp., *Vernonia* spp., *Triticum* spp., *Hordeum* spp., *Oryza* spp., *Avena* spp., *Sorghum* spp., *Secale* spp. and other members of the plant family *Gramineae* ~~not listed~~.

22. (Withdrawn). A plant DNA sequence or part thereof, characterized in that the sequence is substantially homologous to at least a part of SEQ ID NO: 1 or SEQ ID NO: 3, and in that said sequence has been isolated, characterized or designed using a sequence information from SEQ ID NO: 1 or SEQ ID NO: 3, or SEQ ID NO: 1 containing an 81 bp insertion such that the deduced amino acid sequence of the encoded protein contains the repeated sequence SHAGLFNLCVVVLIAVNSRLIENLMK according to SEQ ID NO: 25, where the spacing and identity of the underlined amino acid are identical or are replaced by conserved substitutions.

23. (Currently amended) A method of changing the oil content, acyl composition or diacylglycerol/triacylglycerol ratio of the seed oil of plant seeds, said method comprising: introducing a nucleic acid construct comprising a nucleic acid sequence encoding a polypeptide having diacylglycerol acyltransferase activity into a plant transformation vector; transforming the genome of a plant or plant seed with said plant transformation vector; expressing the nucleic acid sequence; growing the plant or plant seed; and extracting the oil from the plant seed; wherein said polypeptide comprises SEQ ID NO: 2.

24. (Previously presented) The isolated nucleic acid molecule of claim 2, wherein the nucleic acid sequence is SEQ ID NO: 1.

25. (Previously presented) The isolated nucleic acid molecule of claim 2, wherein the nucleic acid sequence is SEQ ID NO: 3.

26. (Previously presented) The vector of claim 4, wherein the nucleic acid sequence is SEQ ID NO: 1.

27. (Previously presented) The vector of claim 4, wherein the nucleic acid sequence is SEQ ID NO: 3.

28. (Previously presented) The plant of claim 10, wherein the introduced nucleotide sequence is SEQ ID NO: 1.

29. (Previously presented) The plant seed of claim 11, wherein the introduced nucleotide sequence is SEQ ID NO: 1.

30. (Previously presented) The method according to claim 19, wherein the nucleotide sequence is SEQ ID NO: 1.

31. (Previously presented) The method according to claim 23, wherein the nucleic acid sequence is SEQ ID NO: 1.

32-33. (Canceled).

34. (New) The plant of claim 10, wherein the plant is selected from the group consisting of consisting of *Arabidopsis thaliana*, *Borago* spp., Canola, *Ricinus* spp., *Theobroma* spp., *Zea* spp., *Gossypium* spp, *Crambe* spp., *Cuphea* spp., *Linum* spp., *Lesquerella* spp., *Limnanthes* spp., Linola, *Tropaeolum* spp., *Oenothera* spp., *Olea* spp., *Elaeis* spp., *Arachis* spp., rapeseed, *Carthamus* spp., *Glycine* spp., *Soja* spp., *Helianthus* spp., *Nicotiana* spp., *Vernonia* spp., *Triticum* spp., *Hordeum* spp., *Oryza* spp., *Avena* spp., *Sorghum* spp., *Secale* spp., Brassicaceae, and other members of the plant family *Gramineae*.

35. (New) The genetically transformed plant of claim 12, wherein the plant is selected from the group consisting of consisting of *Arabidopsis thaliana*, *Borago* spp., Canola, *Ricinus* spp., *Theobroma* spp., *Zea* spp., *Gossypium* spp, *Crambe* spp., *Cuphea* spp., *Linum* spp., *Lesquerella* spp., *Limnanthes* spp., Linola, *Tropaeolum* spp., *Oenothera* spp., *Olea* spp., *Elaeis* spp., *Arachis* spp., rapeseed, *Carthamus* spp., *Glycine* spp., *Soja* spp., *Helianthus* spp., *Nicotiana* spp., *Vernonia* spp., *Triticum* spp., *Hordeum* spp., *Oryza* spp., *Avena* spp., *Sorghum* spp., *Secale* spp., Brassicaceae, and other members of the plant family *Gramineae*.